

RESULT 5
HTONMT
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
FEATURES
source
exon
gene
CDS
intron
exon
intron
exon
BASE COUNT
ORIGIN
Query Match
Best Local Similarity
Matches 1008; Conservative
QY
Db
QY
Db
QY

HTONMT
2072 bp DNA linear PLN 12-APR-1994
Histoplasma capsulatum N-myristoyltransferase (Nmt) exons 1-3,
complete cds.
L25118
L25118.1 GI:407694
N-myristoyltransferase.
Histoplasma capsulatum (strain G217B) DNA.
Ajellomyces capsulatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Onygenaceae; Ajellomyces.
1 (bases 1 to 2072)
Lodge, J.K., Johnson, R.L., Weinberg, R.A. and Gordon, J.I.
Comparison of myristoyl-CoA:protein N-myristoyltransferases from
three pathogenic fungi: Cryptococcus neoformans, Histoplasma
capsulatum, and Candida albicans
J. Biol. Chem. 269 (4), 2996-3009 (1994)
94132075
8300631
Location/Qualifiers
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/organism="Ajellomyces capsulatus"
/strain="G217B"
/db_xref="taxon:5037"
1..715
/number=1
108..1839
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EAVTLDIDDEADVKEFYELLANHYVEDGSAMFRFNYSAPFLNWKALKAPGWKREWHGV
RASKSGKLVASICGVPAAELIAVRGKSLKVTETINFLCVHKKLRSKRLTPVLIKETIRRCY
LNGIYQAIYTVGIMLPTPVSACRYHRALEDWLKLEHVGFSPLPIGSTKSRQVTRNHL
GHTSTPGLRPMQSKDIDAVODLLNRYLKRFDLSQIFSRKEVDHLLHKEKPGAEQIVW
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1567..1641
/gene="Nmt"
/number=2
1642..2072
/number=3
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ACAACCCCGCTCTCAGGAACGAGACGGCGGCATGGACAAAGACAAGGCGGCGGAGGCAA
TGAACCCGCGCCCTACGAAGCGAGCTTGCTGGAATGGATAAGGAAAAGGCAACAGAGAGCTC
TGC GC A A A A A T G A A C A T T G C T G A C A G G C T T G T C A G T T T C C G G G A A G A A C C A G A

106
126
146
166
186
206

RESULT 6			
SPRCg2			
LOCUS	SPRCg2	36493 bp	DNA
DEFINITION	S.pombe chromosome II		linear
ACCESSION	AL022103		PLN 23-MAY-1999
VERSION	AL022103.1	GI:2956767	
KEYWORDS	60S ribosomal protein	116-c: beta transducin	

COMMENT

(URL: <http://www.sanger.ac.uk/projects/S.pombe/>) during 1995 to 1996 about 80% of *S. pombe* chromosome 1 was sequenced by the Sanger Centre. The sequencing of the *S. pombe* genome is now being continued with funding from The European Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project. Protein coding regions (CDS) have been predicted with the help of computer analysis using the GENELINDER program in Pombase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp5splice. CAUTION! It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct splice donor/acceptor sites. CDS are numbered using the following system eg SPBC25H2.01c. SP (S pombe), B (chromosome 2), c25H2 (cosmid name), .01 (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. IMPORTANT! This sequence MAY NOT be the correct sequence.